

Modulating Robo:Ligand Interactions

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CROSS-REFERENCE TO RELATED APPLICATION

10 This application is a continuing application under 35 USC 120 of USSN 60/081,057
filed Apr 07, 1998 and of USSN 60/065,544, filed Nov 14, 1997.

INTRODUCTION

Field of the Invention

The field of this invention is methods for modulating nerve cell function.

Background

15 In the developing CNS, most growth cones confront the midline at one or multiple times during their journey and make the decision of whether to cross or not to cross. This decision is not a static one but rather changes according to the growth cone's history. For example, in the Drosophila ventral nerve cord, about 10% of the interneurons project their axons only on their own side, in some cases extending near the midline without crossing it.
20 The other 90% of the interneurons first project their axons across the midline and then turn to project longitudinally on the other side, often extending near the midline. These growth cones, having crossed the midline once, never cross it again, in spite of their close proximity to the midline and the many commissural axons crossing it. This decision to cross or not to cross is not unique to Drosophila but is common to a variety of midline structures in all
25 bilaterally symmetric nervous systems.

30 What midline signals and growth cone receptors control whether growth cones do or do not cross the midline? After crossing once, what mechanism prevents these growth cones from crossing again? A related issue concerns the nature of the midline as an intermediate target. If so many growth cones find the midline such an attractive structure, why do they cross over it rather than linger? Why do they leave the midline?

One approach to find the genes encoding the components of such a system is to screen for mutations in which either too many or too few axons cross the midline. Such a large-scale mutant screen was previously conducted in *Drosophila*, and led to the identification of two key genes: *commissureless* (*comm*) and *roundabout* (*robo*) (Seeger et al., 1993; reviewed by Tear et al., 1993). In *comm* mutant embryos, commissural growth cones initially orient toward the midline but then fail to cross it and instead recoil and extend on their own side. *robo* mutant embryos, on the other hand, display the opposite phenotype in that too many axons cross the midline; many growth cones that normally extend only on their own side instead now project across the midline and axons that normally cross the midline only once instead appear to cross and recross multiple times (Seeger et al., 1993; present disclosure). Double mutants of *comm* and *robo* display a *robo*-like phenotype.

How do *comm* and *robo* function to control midline crossing? Neither the initial paper on these genes (Seeger et al., 1993) nor the cloning of *comm* (Tear et al., 1996) resolved this question. *comm* encodes a novel surface protein expressed on midline cells. In fact, the *comm* paper (Tear et al., 1996) ended with the hope that future work would "... help shed some light on the enigmatic function of Comm."

USSN 08/971,172 (*Robo, A Novel Family of Polypeptides and Nucleic Acids*, by inventors: Corey S. Goodman, Thomas Kidd, Kevin J. Mitchell and Guy Tear) discloses the cloning and characterization of *robo* in various species including *Drosophila*; Robo polypeptides and polypeptide-encoding nucleic acids are also disclosed and their genbank accession numbers referenced in Kidd et al. (1998) Cell 92, 205-215. *robo* encodes a new class of guidance receptor with 5 immunoglobulin (Ig) domains, 3 fibronectin type III domains, a transmembrane domain, and a long cytoplasmic domain. Robo defines a new subfamily of Ig superfamily proteins that is highly conserved from fruit flies to mammals. The Robo ectodomains, and in particular the first two Ig domains, are highly conserved from fruit fly to human, while the cytoplasmic domains are more divergent. Nevertheless, the cytoplasmic domains contain three highly conserved short proline-rich motifs which may represent binding sites for SH3 or other binding domains in linker or signaling molecules.

For those axons that never cross the midline, Robo is expressed on their growth cones from the outset; for the majority of axons that do cross the midline, Robo is expressed at high levels on their growth cones only after they cross the midline. Transgenic rescue experiments

in *Drosophila* reveal that Robo can function in a cell autonomous fashion, consistent with it functioning as a receptor. Thus, in *Drosophila*, Robo appears to function as the gatekeeper controlling midline crossing; growth cones expressing high levels of Robo are prevented from crossing the midline. Robo proteins in mammals function in a similar manner in controlling axon guidance.

USSN 60/065,54 (*Methods for Modulating Nerve Cell Function*, by inventors: Corey S. Goodman, Thomas Kidd, Guy Tear, Claire Russell and Kevin Mitchell) discloses ectopic and overexpression studies revealing that Comm down-regulates Robo expression, demonstrating that Comm functions to suppress the Robo-mediated midline repulsion. These results show that the levels of Comm at the midline and Robo on growth cones are tightly intertwined and dynamically regulated to assure that only certain growth cones cross the midline, that those growth cones that cross do not linger at the midline, and that once they cross they never do so again.

Relevant Literature

Seeger, M., Tear, G., Ferres-Marco, D. and Goodman C.S. (1993) *Neuron* 10, 409 - 426; Tear G., et al. (1996) *Neuron* 16, 501 - 514; Rothberg et al. (1990) *Genes Dev* 4, 2169-2187; Kidd et al. (1998) *Cell* 92, 205-215.

SUMMARY OF THE INVENTION

The invention provides methods and compositions relating to vertebrate Slit1 and Slit2, collectively vertebrate Slit) polypeptides, related nucleic acids, polypeptide domains thereof having vertebrate Slit-specific structure and activity, and modulators of vertebrate Slit function. Vertebrate Slit polypeptides can regulate cell, especially nerve cell, function and morphology. The polypeptides may be produced recombinantly from transformed host cells from the subject vertebrate Slit polypeptide encoding nucleic acids or purified from mammalian cells. The invention provides isolated vertebrate Slit hybridization probes and primers capable of specifically hybridizing with natural vertebrate Slit genes, vertebrate Slit-specific binding agents such as specific antibodies, and methods of making and using the subject compositions in diagnosis (e.g. genetic hybridization screens for vertebrate Slit transcripts), therapy (e.g. to modulate nerve cell growth) and in the biopharmaceutical industry (e.g. as immunogens, reagents for isolating vertebrate Slit genes and polypeptides,

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reagents for screening chemical libraries for lead pharmacological agents, etc.).

5 The invention also provides methods and compositions for identifying agents which modulate the interaction of Robo and a Robo ligand and for modulating the interaction of Robo and a Robo ligand. The methods for identifying Robo:ligand modulators find particular application in commercial drug screens. These methods generally comprise (1) combining a Robo polypeptide, a Slit polypeptide and a candidate agent under conditions whereby, but for the presence of the agent, the Robo and Slit polypeptides engage in a first interaction, and (2) determining a second interaction of the Robo and Slit polypeptides in the presence of the agent, wherein a difference between the first and second interactions indicates that the agent modulates the interaction of the Robo and Slit polypeptides. The subject methods of modulating the interaction of Robo and a Robo ligand involve combining a Robo polypeptide, a Slit polypeptide and a modulator under conditions whereby, but for the presence of the modulator, the Robo and Slit polypeptides engage in a first interaction, whereby the Robo and Slit polypeptides engage in a second interaction different from the first interaction. In a particular embodiment, the modulator is dominant negative form of the Robo or Slit polypeptide.

DETAILED DESCRIPTION OF THE INVENTION

20 The subject methods include screens for agents which modulate Robo:ligand interactions and methods for modulating Robo:ligand interactions. Robo activation is found to regulate a wide variety of cell functions, including cell-cell interactions, cell mobility, morphology, etc. Slit polypeptides are disclosed as specific activators and inactivators of Robo polypeptides. Accordingly, the invention provides methods for modulating targeted cell function comprising the step of modulating Robo activation by contacting the cell with a modulator of a Robo:Slit interaction..

25 The targeted Robo polypeptide is generally naturally expressed on the targeted cells. The nucleotide sequences of exemplary natural cDNAs encoding drosophila 1, drosophila 2, C. elegans, human 1, human 2 and mouse 1 Robo polypeptides and their translates are described in Kidd et al. (1998) Cell 92, 205-215 and USSN 08/971,172. The targeted Robo polypeptides comprise at least a functional Robo domain, which domain has Robo-specific amino acid sequence and binding specificity or function. Preferred Robo domains comprise

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at least 8, preferably at least 16, more preferably at least 32, most preferably at least 64 consecutive residues of a natural full length Robo. In a particular embodiment, the domains comprise one or more structural/functional Robo immunoglobulin, fibronectin or cytoplasmic motif domains described herein. The subject domains provide Robo-specific antigens and/or immunogens, especially when coupled to carrier proteins. For example, peptides corresponding to Robo- and human Robo-specific domains are covalently coupled to keyhole limpet antigen (KLH) and the conjugate is emulsified in Freund's complete adjuvant. Laboratory rabbits are immunized according to conventional protocol and bled. The presence of Robo-specific antibodies is assayed by solid phase immunosorbant assays using immobilized Robo polypeptides. Generic Robo-specific peptides are readily apparent as conserved regions in aligned Robo polypeptide sequences. In addition, species-specific antigenic and/or immunogenic peptides are readily apparent as diverged extracellular or cytosolic regions in alignments. Human Robo-specific antibodies are characterized as uncross-reactive with non-human Robo polypeptides.

The subject domains provide Robo domain specific activity or function, such as Robo-specific cell, especially neuron modulating or modulating inhibitory activity, Robo-ligand-binding or binding inhibitory activity. Robo-specific activity or function may be determined by convenient *in vitro*, cell-based, or *in vivo* assays: e.g. *in vitro* binding assays, cell culture assays, in animals (e.g. gene therapy, transgenics, etc.), etc. The binding target may be a natural intracellular binding target, a Robo regulating protein or other regulator that directly modulates Robo activity or its localization; or non-natural binding target such as a specific immune protein such as an antibody, or a Robo specific agent such as those identified in screening assays such as described below. Robo-binding specificity may be assayed by binding equilibrium constants (usually at least about 10^7 M^{-1} , preferably at least about 10^8 M^{-1} , more preferably at least about 10^9 M^{-1}), by the ability of the subject polypeptide to function as negative mutants in Robo-expressing cells, to elicit Robo specific antibody in a heterologous host (e.g. a rodent or rabbit), etc.

Similarly, the Slit polypeptide is conveniently selected from Slit polypeptides which specifically activate or inhibit the activation of the Robo polypeptide. Exemplary suitable Slit polypeptides (a) comprises a vertebrate Slit sequence disclosed herein, especially human Slit-1 (SEQ ID NO:02), or a deletion mutant thereof which specifically modulates Robo

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expression or a sequence about 60-70%, preferably about 70-80%, more preferably about 80-90%, more preferably about 90-95%, most preferably about 95-99% similar to a vertebrate Slit sequence disclosed herein as determined by Best Fit analysis using default settings and is other than a natural drosophila Slit sequence, preferably other than a natural invertebrate Slit sequence, and/or (b) is encoded by a nucleic acid comprising a natural Slit encoding sequence (such as a natural human Slit-1 encoding sequence, SEQ ID NO:01) or a fragment thereof at least 36, preferably at least 72, more preferably at least 144, most preferably at least 288 nucleotides in length which specifically hybridizes thereto. Suitable deletion mutants are readily screened in Robo binding or activation assays as described herein. Preferred Slit domains/deletion mutants/^{fragments} comprise at least 8, preferably at least 16, more preferably at least 32, most preferably at least 64 consecutive residues of a disclosed vertebrate Slit sequences and provide a Slit specific activity, such as Slit-specific antigenicity and/or immunogenicity, especially when coupled to carrier proteins as described above for Robo above. Suitable natural Slit encoding sequence fragments are of length sufficient to encode such Slit domains. In a particular embodiment, the Slit fragments comprise species specific fragments; such fragments are readily discerned from alignments of the disclosed sequences, see, e.g. shown as ^{unboxed} ~~white backgrounded~~ sequences in ^{Tables 1 and 2} ~~Tables 3 and 4~~. Exemplary such human Slit-1 immunogenic and/or antigenic peptides are shown in Table ³ ~~1~~.

Table ³ ~~1~~. Immunogenic human Slit-1 polypeptides eliciting Slit-1 specific rabbit polyclonal antibody: Slit polypeptide-KLH conjugates immunized per protocol described above.

<u>Slit Polypeptide</u>	<u>Immunogenicity</u>	<u>Slit Polypeptide</u>	<u>Immunogenicity</u>
SEQ ID NO:02, res. 1-10	+++	SEQ ID NO:02, res. 561-576	+++
SEQ ID NO:02, res. 29-41	+++	SEQ ID NO:02, res. 683-697	+++
SEQ ID NO:02, res. 75-87	+++	SEQ ID NO:02, res. 768-777	+++
SEQ ID NO:02, res. 92-109	+++	SEQ ID NO:02, res. 798-813	+++
SEQ ID NO:02, res. 132-141	+++	SEQ ID NO:02, res. 882-894	+++
SEQ ID NO:02, res. 192-205	+++	SEQ ID NO:02, res. 934-946	+++
SEQ ID NO:02, res. 258-269	+++	SEQ ID NO:02, res. 1054-1067	+++
SEQ ID NO:02, res. 295-311	+++	SEQ ID NO:02, res. 1181-1192	+++
SEQ ID NO:02, res. 315-330	+++	SEQ ID NO:02, res. 1273-1299	+++
SEQ ID NO:02, res. 373-382	+++	SEQ ID NO:02, res. 1383-1397	+++
SEQ ID NO:02, res. 403-422	+++	SEQ ID NO:02, res. 1468-1477	+++
SEQ ID NO:02, res. 474-485	+++	SEQ ID NO:02, res. 1508-1517	+++

The subject domains provide Slit domain specific activity or function, such as Slit-

specific cell, especially neuron modulating or modulating inhibitory activity, Slit-ligand-binding or binding inhibitory activity. Slit-specific activity or function may be determined by convenient *in vitro*, cell-based, or *in vivo* assays: e.g. *in vitro* binding assays, cell culture assays, in animals (e.g. gene therapy, transgenics, etc.), etc. The binding target may be a natural intracellular binding target, a Slit regulating protein or other regulator that directly modulates Slit activity or its localization; or non-natural binding target such as a specific immune protein such as an antibody, or a Slit specific agent such as those identified in screening assays such as described below. Slit-binding specificity may be assayed by binding equilibrium constants (usually at least about 10^7 M^{-1} , preferably at least about 10^8 M^{-1} , more preferably at least about 10^9 M^{-1}), by the ability of the subject polypeptide to function as negative mutants in Slit-expressing cells, to elicit Slit specific antibody in a heterologous host (e.g a rodent or rabbit), etc.

In one embodiment, the Slit polypeptides are encoded by a nucleic acid comprising SEQ ID NO:01 or a fragment thereof which hybridizes with a full-length strand thereof, preferably under stringent conditions. Such nucleic acids comprise at least 36, preferably at least 72, more preferably at least 144 and most preferably at least 288 nucleotides of SEQ ID NO:01. Demonstrating specific hybridization generally requires stringent conditions, for example, hybridizing in a buffer comprising 30% formamide in 5 x SSPE (0.18 M NaCl, 0.01 M NaPO_4 , pH7.7, 0.001 M EDTA) buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with 0.2 x SSPE (Conditions I); preferably hybridizing in a buffer comprising 50% formamide in 5 x SSPE buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with 0.2 x SSPE buffer at 42°C (Conditions II). Exemplary nucleic acids which hybridize with a strand of SEQ ID NO:01 are shown in Table ~~2~~⁴.

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Table 7. Exemplary nucleic acids which hybridize with a strand of SEQ ID NO:01 under Conditions I and/or II.

	<u>Slit Nucleic Acid</u>	<u>Hybridization</u>	<u>Slit Nucleic Acid</u>	<u>Hybridization</u>
5	SEQ ID NO:01, nucl. 1-47	+	SEQ ID NO:01, nucl. 1258-1279	+
	SEQ ID NO:01, nucl. 58-99	+	SEQ ID NO:01, nucl. 1375-1389	+
	SEQ ID NO:01, nucl. 95-138	+	SEQ ID NO:01, nucl. 1581-1595	+
	SEQ ID NO:01, nucl. 181-220	+	SEQ ID NO:01, nucl. 1621-1639	+
	SEQ ID NO:01, nucl. 261-299	+	SEQ ID NO:01, nucl. 1744-1755	+
	SEQ ID NO:01, nucl. 274-315	+	SEQ ID NO:01, nucl. 1951-1969	+
10	SEQ ID NO:01, nucl. 351-389	+	SEQ ID NO:01, nucl. 2150-2163	+
	SEQ ID NO:01, nucl. 450-593	+	SEQ ID NO:01, nucl. 2524-2546	+
	SEQ ID NO:01, nucl. 524-546	+	SEQ ID NO:01, nucl. 2761-2780	+
	SEQ ID NO:01, nucl. 561-608	+	SEQ ID NO:01, nucl. 2989-2999	+
	SEQ ID NO:01, nucl. 689-727	+	SEQ ID NO:01, nucl. 3108-3117	+
15	SEQ ID NO:01, nucl. 708-737	+	SEQ ID NO:01, nucl. 3338-3351	+
	SEQ ID NO:01, nucl. 738-801	+	SEQ ID NO:01, nucl. 3505-3514	+
	SEQ ID NO:01, nucl. 805-854	+	SEQ ID NO:01, nucl. 3855-3867	+
	SEQ ID NO:01, nucl. 855-907	+	SEQ ID NO:01, nucl. 4010-4025	+
	SEQ ID NO:01, nucl. 910-953	+	SEQ ID NO:01, nucl. 4207-4219	+
20	SEQ ID NO:01, nucl. 1007-1059	+	SEQ ID NO:01, nucl. 4333-4345	+
	SEQ ID NO:01, nucl. 1147-1163	+	SEQ ID NO:01, nucl. 4521-4529	+

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A wide variety of cell types express Robo polypeptides subject to regulation by the disclosed methods, including many neuronal cells, transformed cells, infected (e.g. virus) cells, etc. Ascertaining Robo binding or activation is readily effected by binding assays or cells function assays as disclosed herein or in the cited copending applications. Accordingly, indications for the subject methods encompass a wide variety of cell types and function, including axon outgrowth, tumor cell invasion or migration, etc. The target cell may reside in culture or in situ, i.e. within the natural host. For in situ applications, the compositions are added to a retained physiological fluid such as blood or synovial fluid. For CNS administration, a variety of techniques are available for promoting transfer of the therapeutic across the blood brain barrier including disruption by surgery or injection, drugs which transiently open adhesion contact between CNS vasculature endothelial cells, and compounds which facilitate translocation through such cells. Slit polypeptides may also be amenable to direct injection or infusion, topical, intratracheal/nasal administration e.g. through aerosol, intraocularly, or within/on implants e.g. fibers e.g. collagen, osmotic pumps, grafts comprising appropriately transformed cells, etc. A particular method of administration involves coating, embedding or derivatizing fibers, such as collagen fibers, protein polymers,

etc. with therapeutic polypeptides. Other useful approaches are described in Otto et al. (1989) J Neuroscience Research 22, 83-91 and Otto and Unsicker (1990) J Neuroscience 10, 1912-1921. Generally, the amount administered will be empirically determined, typically in the range of about 10 to 1000 $\mu\text{g/kg}$ of the recipient and the concentration will generally be in the range of about 50 to 500 $\mu\text{g/ml}$ in the dose administered. Other additives may be included, such as stabilizers, bactericides, etc. will be present in conventional amounts.

In one embodiment, the invention provides administering the subject Slit polypeptides in combination with a pharmaceutically acceptable excipient such as sterile saline or other medium, gelatin, an oil, etc. to form pharmaceutically acceptable compositions. The compositions and/or compounds may be administered alone or in combination with any convenient carrier, diluent, etc. and such administration may be provided in single or multiple dosages. Useful carriers include solid, semi-solid or liquid media including water and non-toxic organic solvents. In another embodiment, the invention provides the subject compounds in the form of a pro-drug, which can be metabolically converted to the subject compound by the recipient host. A wide variety of pro-drug formulations for polypeptide-based therapeutics are known in the art. The compositions may be provided in any convenient form including tablets, capsules, troches, powders, sprays, creams, etc. As such the compositions, in pharmaceutically acceptable dosage units or in bulk, may be incorporated into a wide variety of containers. For example, dosage units may be included in a variety of containers including capsules, pills, etc. The compositions may be advantageously combined and/or used in combination with other therapeutic or prophylactic agents, different from the subject compounds. In many instances, administration in conjunction with the subject compositions enhances the efficacy of such agents, see e.g. *Goodman & Gilman's The Pharmacological Basis of Therapeutics*, 9th Ed., 1996, McGraw-Hill.

In another aspect, the invention provides methods of screening for agents which modulate Robo-Slit interactions. These methods generally involve forming a mixture of a Robo-expressing cell, a Slit polypeptide and a candidate agent, and determining the effect of the agent on the amount of Robo expressed by the cell. The methods are amenable to automated, cost-effective high throughput screening of chemical libraries for lead compounds. Identified reagents find use in the pharmaceutical industries for animal and

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human trials; for example, the reagents may be derivatized and rescreened in *in vitro* and *in vivo* assays to optimize activity and minimize toxicity for pharmaceutical development. Cell and animal based neural guidance/repulsion assays are described in detail in the experimental section below.

5 The amino acid sequences of the disclosed vertebrate Slit polypeptides are used to back-translate Slit polypeptide-encoding nucleic acids optimized for selected expression systems (Holler et al. (1993) Gene 136, 323-328; Martin et al. (1995) Gene 154, 150-166) or used to generate degenerate oligonucleotide primers and probes for use in the isolation of natural Slit-encoding nucleic acid sequences ("GCG" software, Genetics Computer Group, 10 Inc, Madison WI). Slit-encoding nucleic acids used in Slit-expression vectors and incorporated into recombinant host cells, e.g. for expression and screening, transgenic animals, e.g. for functional studies such as the efficacy of candidate drugs for disease associated with Slit-modulated cell function, etc.

15 The invention also provides nucleic acid hybridization probes and replication / amplification primers having a vertebrate Slit cDNA specific sequence comprising a fragment of a disclosed vertebrate cDNA sequence, and sufficient to effect specific hybridization thereto. Such primers or probes are at least 12, preferably at least 24, more preferably at least 36 and most preferably at least 96 nucleotides in length. Demonstrating specific hybridization generally requires stringent conditions, for example, hybridizing in a buffer 20 comprising 30% formamide in 5 x SSPE (0.18 M NaCl, 0.01 M NaPO₄, pH7.7, 0.001 M EDTA) buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with 0.2 x SSPE; preferably hybridizing in a buffer comprising 50% formamide in 5 x SSPE buffer at a temperature of 42°C and remaining bound when subject to washing at 42°C with 0.2 x SSPE buffer at 42°C. Slit nucleic acids can also be distinguished using alignment 25 algorithms, such as BLASTX (Altschul *et al.* (1990) Basic Local Alignment Search Tool, J Mol Biol 215, 403-410). In addition, the invention provides nucleic acids having a sequence about 60-70%, preferably about 70-80%, more preferably about 80-90%, more preferably about 90-95%, most preferably about 95-99% similar to a vertebrate Slit sequence disclosed herein as determined by Best Fit analysis using default settings and is other than a natural 30 drosophila Slit sequence, preferably other than a natural invertebrate Slit sequence. In a particular embodiment, the Slit polynucleotide fragments comprise species specific

fragments; such fragments are readily discerned from alignments of the disclosed sequences.

The subject nucleic acids are of synthetic/non-natural sequences and/or are recombinant, meaning they comprise a non-natural sequence or a natural sequence joined to nucleotide(s) other than that which it is joined to on a natural chromosome. The subject recombinant nucleic acids comprising the nucleotide sequence of disclosed vertebrate Slit nucleic acids, or fragments thereof, contain such sequence or fragment at a terminus, immediately flanked by (i.e. contiguous with) a sequence other than that which it is joined to on a natural chromosome, or flanked by a native flanking region fewer than 10 kb, preferably fewer than 2 kb, more preferably fewer than 500 bp, which is at a terminus or is immediately flanked by a sequence other than that which it is joined to on a natural chromosome. While the nucleic acids are usually RNA or DNA, it is often advantageous to use nucleic acids comprising other bases or nucleotide analogs to provide modified stability, etc.

The subject nucleic acids find a wide variety of applications including use as translatable transcripts, hybridization probes, PCR primers, diagnostic nucleic acids, etc.; use in detecting the presence of Slit genes and gene transcripts and in detecting or amplifying nucleic acids encoding additional Slit homologs and structural analogs. In diagnosis, Slit hybridization probes find use in identifying wild-type and mutant Slit alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific oligonucleotide (ASO) probes for high-throughput clinical diagnoses. In therapy, therapeutic Slit nucleic acids are used to modulate cellular expression or intracellular concentration or availability of active Slit. Exemplary human Slit-1 probes and primers are shown in Table 5 (~~A and B~~) and Table

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The following exemplary assay is offered by way of illustration and not by way of limitation:

EXAMPLES

Protocol for Ligand Screening of Transfected COS cells.

I. Prepare the Ligand

Expression Construct: cDNAs encoding targeted Slit polypeptides are tagged with the Fc portion of human IgG and subcloned into a 293 expression vector (pCEP4: In Vitrogen).

Transfection: 293 EBNA cells are transfected (CaPO₄ method) with the Slit

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expression constructs. After 24 h recovery, transfected cells are selected with G418 (geneticin, 250 ug/ml, Gibco) and hygromycin (200 ug/ml). Once the selection process is complete, cells are maintained in Dulbecco's Modified Eagles medium (DME)/10% FCS under selection.

5 Preparation of Conditioned Medium: Serum-containing media is replaced with Optimem with glutamax-1 (Gibco) and 300 ng/ml heparin (Sigma), and the cells are conditioned for 3 days. The media is collected and spun at 3,000xg for 10 minutes. The supernatant is filtered (0.45 um) and stored with 0.1% azide at 4°C for no more than 2 weeks.

10 II. Prepare Truncated Receptor (Positive Control)

Expression Construct: cDNA encoding a corresponding Robo C-terminal deletion mutant comprising the extracellular domain (truncated immediately N-terminal to the transmembrane region) is subcloned into a 293 expression vector (pCEP4: In Vitrogen).

Transfection: 293 EBNA cells are transfected (CaPO₄ method) with the receptor mutant expression construct. After 24 h recovery, transfected cells are selected with G418 (geneticin, 250 ug/ml, Gibco) and hygromycin (200 ug/ml). Once the selection process is complete, cells are maintained in Dulbecco's Modified Eagles medium (DME)/10% FCS under selection.

Preparation of Conditioned Medium: Serum-containing media is replaced with Optimem with glutamax-1 (Gibco) and 300 ng/ml heparin (Sigma), and the cells are conditioned for 3 days. The media is collected and spun at 3,000xg for 10 minutes. The supernatant is filtered (0.45 um) and stored with 0.1% azide at 4°C for no more than 2 weeks.

20 II. Transfect COS Cells

Seed COS cells (250,000) on 35 mm dishes in 2 ml DME/10% FCS.

18-24 h later, dilute 1 ug of Robo-encoding DNA (cDNA cloned into pMT21 expression vector) into 200 ul serum-free media and add 6 ul of Lipofectamine (Gibco). Incubate this solution at room temperature for 15-45 min.

Wash the cells 2X with PBS. Add 800 ul serum-free media to the tube containing the lipid-DNA complexes. Overlay this solution onto the washed cells.

Incubate for 6 h. Stop the reaction by adding 1 ml DMA/20% FCS. Refeed cells.

30 Assay cells 12 hr later.

III. Ligand Binding Assay

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Wash plates of transfected COS cells 1X with cold PBS (plus Ca/Mg)/1% goat serum.
Add 1 ml conditioned media neat and incubate 90 min at room temp.

Wash plates 3X with PBS (plus Ca/Mg). On the 4th wash, add 1 ml 50% methanol to 1 ml PBS. Then add 1 ml methanol. Evacuate and add 1 ml methanol.

5 Wash 1X with PBS. Wash 1X PBS/1% goat serum.

Add secondary antibody (1-to-2,000 anti-human Fc conjugated to alkaline phosphatase (Jackson Lab)) in PBS/1% goat serum. Incubate 30-40 min room temp.

10 Wash 3X with PBS. Wash 1X alkaline phosphatase buffer (100 mM Tris-Cl, pH 9.5, 100 mM NaCl, 5 mM MgCl₂). Prepare alkaline phosphatase reagents: 4.5 ul/ml NBT and 3.5 ul/ml BCIP (Gibco) in alkaline phosphatase buffer.

Incubate 10-30 min, quench with 20 mM EDTA in PBS. Cells that have bound Slit polypeptides are visible by the presence of a dark purple reaction product.

In parallel incubations, positive controls are provided by titrating Slit binding with serial dilutions of the mutant receptor conditioned medium.

15 IV. Results: Binding of Slit to Robo

Cell expressing mammalian Slit polypeptides were shown to bind Robo. No reactivity was observed with control COS cells or with receptor-expressing COS cells in the presence of the secondary antibody but in the absence of the Slit-Fc fusion. Binding was observed to receptor-expression cells using a construct in which a Slit polypeptide is fused directly to alkaline phosphatase, for which a secondary antibody is not required. Receptor deletion mutants titrate the Slit-Robo binding, serving as a positive control for inhibition assays.

Protocol for high throughput Robo-Slit binding assay.

25 A. Reagents:

- Neutralite Avidin: 20 µg/ml in PBS.
- Blocking buffer: 5% BSA, 0.5% Tween 20 in PBS; 1 hour at room temperature.
- Assay Buffer: 100 mM KCl, 20 mM HEPES pH 7.6, 1 mM MgCl₂, 1% glycerol, 0.5% NP-40, 50 mM β-mercaptoethanol, 1 mg/ml BSA, cocktail of protease inhibitors.
- ³³P Robo polypeptide 10x stock: 10⁻⁸ - 10⁻⁶ M "cold" Robo polypeptide specific Robo domain supplemented with 200,000-250,000 cpm of labeled Robo (Beckman counter). Place in the 4°C microfridge during screening.

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- Protease inhibitor cocktail (1000X): 10 mg Trypsin Inhibitor (BMB # 109894), 10 mg Aprotinin (BMB # 236624), 25 mg Benzamidine (Sigma # B-6506), 25 mg Leupeptin (BMB # 1017128), 10 mg APMSF (BMB # 917575), and 2mM NaVO₃ (Sigma # S-6508) in 10 ml of PBS.

5 - Slit: 10⁻⁷ - 10⁻⁵ M biotinylated Slit in PBS.

B. Preparation of assay plates:

- Coat with 120 µl of stock N-Avidin per well overnight at 4°C.

- Wash 2 times with 200 µl PBS.

- Block with 150 µl of blocking buffer.

10 - Wash 2 times with 200 µl PBS.

C. Assay:

- Add 40 µl assay buffer/well.

- Add 10 µl compound or extract.

- Add 10 µl ³³P-Robo (20-25,000 cpm/0.1-10 pmoles/well = 10⁻⁹ - 10⁻⁷ M final conc).

15 - Shake at 25°C for 15 minutes.

- Incubate additional 45 minutes at 25°C.

- Add 40 µM biotinylated Slit (0.1-10 pmoles/40 ul in assay buffer)

- Incubate 1 hour at room temperature.

- Stop the reaction by washing 4 times with 200 µM PBS.

20 - Add 150 µM scintillation cocktail.

- Count in Topcount.

D. Controls for all assays (located on each plate):

a. Non-specific binding

b. Soluble (non-biotinylated Slit) at 80% inhibition.

25 All publications and patent applications cited in this specification are herein
incorporated by reference as if each individual publication or patent application were
specifically and individually indicated to be incorporated by reference. Although the
foregoing invention has been described in some detail by way of illustration and example for
purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in
30 the art in light of the teachings of this invention that certain changes and modifications may
be made thereto without departing from the spirit or scope of the appended claims.

15

SEQ 10 NO: 1

SEQ 10 NO: 1

Sequence of Human Slit-1

SEQ 10 NO: 2

DNA sequence and predicted protein product. Base pair and amino acid number are indicated on the right hand side.

ATGCGCGCGTTGGCTGGCAGATGCTGTCCCTGTCGCTGGGGTTAGTGTGGCGATCCTGAACAAGGTGGCACCG 75
M R G V G W Q M L S L S L G L V L A I L N K V A P 25

CAGGCGTGCCCGCGCAGTGTCTTGTCTCGGGCAGCACAGTGGACTGTACGGGCTGGCGCTGCGCAGCGTGCCC 150
Q A C P A Q C S C S G S T V D C H G L A L R S V P 50

AGGAATATCCCCCGAACACCGAGAGACTGGATTAAATGGAAATAACATCACAGAATTACGAAGACAGATTTT 225
R N I P R N T E R L D L N G N N I T R I T K T D F 75

GCTGGTCTTAGACATCTAAGAGTTCTTCAGCTTATGGAGAATAAGATTAGCACCATTGAAAGAGGAGCATTCCAG 300
A G L R H L R V L Q L M E N K I S T I E R G A F Q 100

GATCTTAAAGAACTAGAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTTCCTGAGTTGCTGTTTCTGGG 375
D L K E L E R L R L N R N H L Q L F P E L L F L G 125

ACTGCGAAGCTATACAGGCTTGATCTCAGTGAACCAAAATTCAGGCAATCCCAAGGAAAGCTTCCGTGGGGCA 450
T A K L Y R L D L S E N Q I Q A I P R K A F R G A 150

GTTGACATAAAAAATTTGCAACTGGATTACAACCAGATCAGCTGTATTGAAGATGGGGCATTGAGGGCTCTCCGG 525
V D I K N L Q L D Y N Q I S C I E D G A F R A L R 175

GACCTGGAAGTGCTCACTCTCAACAATAACAACATTACTAGACTTTCTGTGGCAAGTTTCAACCATATGCCTAAA 600
D L E V L T L N N N N I T R L S V A S F N H M P K 200

CTTAGGACTTTTCGACTGCATTCAAACAACCTGTATTGTGACTGCCACCTGGCCTGGCTCTCCGACTGGCTTCGC 675
L R T F R L H S N N L Y C D C H L A W L S D W L R 225

AAAAGGCTCGGGTTGGTCTGTACACTCAGTGTATGGGCCCCCTCCACCTGAGAGGCCATAATGTAGCCGAGGTT 750
K R P R V G L Y T Q C M G P S H L R G H N V A E V 250

CAAAAACGAGAATTTGTCTGCAGTGATGAGGAAGAAGGTCACCAGTCATTATGGCTCCTTCTGTAGTGTTTTG 825
Q K R E F V C S D E E E G H Q S F M A P S C S V L 275

CACTGCCCTGCCGCTGTACCTGTAGCAACAATATCGTAGACTGTCTGTGGGAAAGGTCTCACTGAGATCCCCACA 900
H C P A A C T C S N N I V D C R G K G L T E I P T 300

AATCTTCCAGAGACCATCACAGAAATACGTTTGGAACAGAACACAATCAAAGTCATCCCTCCTGGAGCTTTCTCA 975
N L P E T I T E I R L E Q N T I K V I P P G A F S 325

CCATATAAAAAGCTTAGACGAATTGACCTGAGCAATAATCAGATCTCTGAACTTGACCAGATGCTTTCCAAGGA 1050
P Y K K L R R I D L S N N Q I S E L A P D A F Q G 350

CTACGCTCTCTGAATTCACCTGTCTCTATGGAAATAAAATCACAGAACTCCCCAAAAGTTTATTTGAAGGACTG 1125
L R S L N S L V L Y G N K I T E L P K S L F E G L 375

TTTTCTTACAGCTCCTATTATTGAATGCCAACAAGATAAACTGCCTTCGGGTAGATGCTTTTCAGGATCTCCAC 1200
F S L Q L L L L N A N K I N C L R V D A F Q D L H 400

AACTTGACCTTCTCTCCCTATATGACAACAAGCTTCAGACCATCGCCAAGGGGACCTTTTCACCTCTTCGGGCC 1275
N L N L L S L Y D N K L Q T I A K G T F S P L R A 425

ATTCAAACTATGCATTGGCCCCAGAACCCTTTATTTGTGACTGCCATCTCAAGTGGCTAGCGGATTATCTCCAT 1350
I Q T M H L A Q N P F I C D C H L K W L A D Y L H 450

ACCAACCCGATTGAGACCAAGTGGTGGCCGTTGCACCAGCCCCCGCCGCTGGCAAACAAAAGAATTGGACAGATC 1425
T N P I E T S G A R C T S P R R L A N K R I G Q I 475

AAAAGCAAGAAATTCGTTGTTTCAGGTACAGAAGATTATCGATCAAAATTAAGTGGAGACTGCTTTGCGGATCTG 1500
K S K K F R C S G T E D Y R S K L S G D C F A D L 500

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GCTTGCCCTGAAAAGTGTGCTGTGAAGGAACACAGTAGATTGCTCTAATCAAAAGCTCAACAAAATCCCGGAG	1575
A C P E K C R C E G T T V D C S N Q K L N K I P E	525
CACATTCCCCAGTACACTGCAGAGTTGCGTCTCAATAATAATGAATTTACCGTGTGGAAGCCACAGGAATCTTT	1650
H I P Q Y T A E L R L N N N E F T V L E A T G I F	550
AAGAACTTCTCTCAATTACGTAAAATAAACTTTAGCAACAATAAGATCACAGATATTGAGGAGGGAGCATTTGAA	1725
K K L P Q L R K I N F S N N K I T D I E E G A F E	575
GGAGCATCTGGTGTAATGAAATACTTCTTACGAGTAATCGTTTGGAAAATGTGCAGCATAAGATGTTCAAGGGA	1800
G A S G V N E I L L T S N R L E N V Q H K M F K G	600
TTGGAAGCCCTCAAACTTTGATGTTGAGAAGCAATCGAATAACCTGTGTGGGAATGACAGTTTCATAGGACTC	1875
L E S L K T L M L R S N R I T C V G N D S F I G L	625
AGTTCTGTGCGTTTGCTTTCTTTGTATGATAATCAAATTACTACAGTTGCACCAGGGGCATTGATACTCTCCAT	1950
S S V R L L S L Y D N Q I T T V A P G A F D T L H	650
TCTTTATCTACTCTAAACCTCTTGGCCAATCCTTTTAACTGTAACCTGCTACCTGGCTTGGTTGGGAGAGTGGCTG	2025
S L S T L N L L A N P F N C N C Y L A W L G E W L	675
AGAAAGAAGAGAATTGTACGCGGAAATCCTAGATGTCAAAAACCATACTTCTGAAAGAAATACCCATCCAGGAT	2100
R K K R I V T G N P R C Q K P Y F L K E I P I Q D	700
GTGGCCATTACAGGACTTCACTTGTGATGACGGAATGATGACAAATAGTTGCTCCCACTTTCTCGCTGTCTACT	2175
V A I Q D F T C D D G N D D N S C S P L S R C P T	725
GAATGTACTTGTGTTGATACAGTCCGATGTAGCAACAGGGTTTGAAGGTCTTGCCGAAAGGTATTCCAAGA	2250
E C T C L D T V V R C S N K G L K V L P K G I P R	750
GATGTCACAGAGTTGTATCTGGATGGAACCAATTTACACTGGTTCCCAAGGAACTCTCCAACCTACAAACATTTA	2325
D V T E L Y L D G N Q F T L V P K E L S N Y K H L	775
ACACTTATAGACTTAAGTAACAACAGAATAAGCAGCTTTCTAATCAGAGCTTCAGCAACATGACCCAGCTCCTC	2400
T L I D L S N N R I S T L S N Q S F S N M T Q L L	800
ACCTTAATCTTAGTTACAACCGTCTGAGATGTATTCTCTCGCACCTTTGATGGATTAAAGTCTCTTCGATTA	2475
T L I L S Y N R L R C I P P R T F D G L K S L R L	825
CTTTCTCTACATGGAATGACATTTCTGTTGTGCTGAAGGTGCTTTCAATGATCTTTCTGCATTATCACATCTA	2550
L S L H G N D I S V V P E G A F N D L S A L S H L	850
GCAATTGGAGCCAACCTCTTACTGTGATTGTAACATGCAGTGGTTATCCGACTGGGTGAAGTCGGAATATAAG	2625
A I G A N P L Y C D C N M Q W L S D W V K S E Y K	875
GAGCCTGGAATTGCTCGTTGTGCTGGTCTGGAGAAATGGCAGATAAACTTTTACTCACAACCTCCCTCCAAAAA	2700
E P G I A R C A G P G E M A D K L L L T T P S K K	900
TTTACCTGTCAAGTCTGTGGATGTCAATATTCTAGCTAAGTGAACCCCTGCCTATCAAATCCGTGTAAAAAT	2775
F T C Q G P V D V N I L A K C N P C L S N P C K N	925
GATGGCACATGTAATAGTGATCCAGTTGACTTTTACCGATGCACCTGTCCATATGGTTTCAAGGGGCAGGACTGT	2850
D G T C N S D P V D F Y R C T C P Y G F K G Q D C	950
GATGTCCCAATTCATGCCTGCATCAGTAACCCATGTAAACATGGAGGAACTTGCCACTTAAAGGAAGGAGAAGAA	2925
D V P I H A C I S N P C K H G G T C H L K E G E E	975
GATGGATTCTGGTGATTGTTGTGCTGATGGATTGTAAGGAGAAAATTGTGAAGTCAACGTTGATGATTGTGAAGAT	3000
D G F W C I C A D G F E G E N C E V N V D D C E D	1000
AATGACTGTGAAAATAATTCTACATGTGTCGATGGCATTAACTACACATGCCTTTGCCACCTGAGTATACA	3075
N D C E N N S T C V D G I N N Y T C L C P P E Y T	1025

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GGTGAGTTGTGTGAGGAGAAGCTGGACTTCTGTGCCCAGGACCTGAACCCCTGCCAGCACGATTCAAAGTGCATC 3150
G E L C E E K L D F C A Q D L N P C Q H D S K C I 1050

CTAACTCCAAAGGGATTCAAATGTGACTGCACACCAGGGTACGTAGGTGAACACTGCGACATCGATTTTGACGAC 3225
L T P K G F K C D C T P G Y V G E H C D I D F D D 1075

TGCCAAGACAACAAGTGTA AAAACGGAGCCCACTGCACAGATGCAGTGAACGGCTATACGTGCATATGCCCCGAA 3300
C Q D N K C K N G A H C T D A V N G Y T C I C P E 1100

GGTTACAGTGGCTTGTCTGTGAGTTTCTCCACCCATGGTCCTCCCTCGTACCAGCCCTGTGATAATTTTGAT 3375
G Y S G L F C E F S P P M V L P R T S P C D N F D 1125

TGTCAGAATGGAGCTCAGTGTATCGTCAGAATAAATGAGCCAATATGTCAGTGTTCCTGGCTATCAGGGAGAA 3450
C Q N G A Q C I V R I N E P I C Q C L P G Y Q G E 1150

AAGTGTGAAAAATTGGTTAGTGTGAATTTTATAAACAAGAGTCTTATCTTCAGATTCCCTCAGCCAAGGTTCCG 2525
K C E K L V S V N F I N K E S Y L Q I P S A K V R 1175

CCTCAGACGAACATAACACTTCAGATTGCCACAGATGAAGACAGCGGAATCCTCCTGTATAAGGGTGACAAAGAC 3600
P Q T N I T L Q I A T D E D S G I L L Y K G D K D 1200

CATATCGCGGTAGAACTCTATCGGGGGCGTGTCTGTGCCAGCTATGACACCGGCTCTCATCCAGCTTCTGCCATT 3675
H I A V E L Y R G R V R A S Y D T G S H P A S A I 1225

TACAGTGTGGAGACAATCAATGATGGAAACTTCCACATTGTGGAACACTTGCCTTGGATCAGAGTCTCTCTTTG 3750
Y S V E T I N D G N F H I V E L L A L D Q S L S L 1250

TCCGTGGATGGTGGGAACCCCAAAATCATCTAACTTGTCAAAGCAGTCCACTCTGAATTTTGACTCTCCACTC 3825
S V D G G N P K I I T N L S K Q S T L N F D S P L 1275

TATGTAGGAGGCATGCCAGGGAAGAGTAACGTGGCATCTCTGCGCCAGGCCCTGGGCAGAACGGAACCAGCTTC 3900
Y V G G M P G K S N V A S L R Q A P G Q N G T S F 1300

CACGGCTGCATCCGGAACCTTTACATCAACAGTGAGCTGCAGGACTTCCAGAAGGTGCCGATGCAAACAGGCATT 3975
H G C I R N L Y I N S E L Q D F Q K V P M Q T G I 1325

TTGCCTGGCTGTGAGCCATGCCACAAGAAGGTGTGTGCCCATGGCACATGCCAGCCCAGCAGCCAGGCAGGCTTC 4050
L P G C E P C H K K V C A H G T C Q P S S Q A G F 1350

ACCTGCGAGTGCCAGGAAGGATGGATGGGGGCCCTCTGTGACCAACGGACCAATGACCCTTGCCCTTGAAATAAA 4125
T C E C Q E G W M G P L C D Q R T N D P C L G N K 1375

TGCGTACATGGCACCTGCTTGCCCATCAATGCGTTCTCTACAGCTGTAAGTGCTTGGAGGGCCATGGAGGTGTC 4200
C V H G T C L P I N A F S Y S C K C L E G H G G V 1400

CTCTGTGATGAAGAGGAGGATCTGTTTAAACCATGCCAGCGATCAAGTGCAAGCATGGGAAGTGAGGCTTTCA 4275
L C D E E E D L F N P C Q A I K C K H G K C R L S 1425

GGTCTGGGGCAGCCCTACTGTGAATGCAGCAGTGGATACCGGGGGACAGCTGTGATCGAGAAATCTCTTGTCGA 4350
G L G Q P Y C E C S S G Y T G D S C D R E I S C R 1450

GGGGAAGGATAAGAGATTATTACCAAAAAGCAGCAGGGCTATGCTGCTTGCCAAACAACCAAGAAGGTGTCCCGA 4425
G E R I R D Y Y Q K Q Q G Y A A C Q T T K K V S R 1475

TTAGAGTGCAGAGGTGGGTGTGCAGGAGGGCAGTGTGTGGACCGCTGAGGAGCAAGCGGCGAAATACTCTTTTC 4500
L E C R G G C A G G Q C C G P L R S K R R K Y S F 1500

GAATGCACTGACGGCTCCTCCTTTGTGGACGAGGTTGAGAAAGTGGTGAAGTGCAGGCTGTACGAGGTGTGTGCC 4575
E C T D G S S F V D E V E K V V K C G C T R C V S 1525

Features of Human Slit-1 predicted protein

Co-ordinates refer to amino acid number.

Signal sequence:	7-24	
First amino-flanking sequence:	28-59	
First set of Leucine Rich Repeats:	60-179	(6 repeats)
First carboxy-flanking sequence:	180-276	
Second amino-flanking sequence:	277-308	
Second set of Leucine Rich Repeats:	309-434	(5 repeats)
Second carboxy-flanking sequence:	435-501	
Third amino-flanking sequence:	502-533	
Third set of Leucine Rich Repeats:	534-660	(5 repeats)
Third carboxy-flanking sequence:	661-722	
Fourth amino-flanking sequence:	723-754	
Fourth set of Leucine Rich Repeats:	755-855	(4 repeats)
Fourth carboxy-flanking sequence:	856-917	
First EGF repeat:	918-952	
Second EGF repeat:	953-993	
Third EGF repeat:	994-1031	
Fourth EGF repeat:	1032-1071	
Fifth EGF repeat:	1072-1109	
Spacer:	1110-1116	
Sixth EGF repeat:	1117-1154	
"99aa spacer":	1155-1329	
Seventh EGF repeat:	1330-1366	
Eighth EGF repeat:	1367-1404	
Nineth EGF repeat:	1405-1447	
Cysteine knot motif:	1448-1525	

Leucine rich repeats (LRRs) are predicted by comparison with known proteins and by the presence of the core sequence: xxxFxxLxxLxxLxLxxNxIxxL, where x is any amino acid. In slit proteins, the LRRs are flanked by conserved sequences referred to as the amino- and carboxy- flanking regions. These flanking regions are found in other known proteins, but only in a few instances are both the amino- and carboxy- flank regions present in a single protein. The amino flank region is defined by the consensus: CPxxCx C[1-6x]GxxVDCxxxGL[2-4x] α Pxx α Pxdttx where x is any amino acid, [x] represents a variable number of amino acids and α is a hydrophobic residue. Lower case indicates a residue is not highly conserved at a particular position. The carboxy flank region is defined by the consensus: P β xC γ Cx α [1-5x]W α [14-26x]RCxxPxxxxxxx α xxxxxF[1-3x]Cs[3-17x] where β is W or a hydrophobic residue, γ is D or N and α is a hydrophobic residue.

Epidermal growth factor (EGF) repeats are predicted by the consensus: CxxxxCxngxC[6-9x] α CxCxxGxxGxxCxxxxxx.

The so called "99aa spacer" is actually ~200 amino acids in the Drosophila protein and 174 amino acids in Human Slit-1. This region shows homology to the G-loops of laminin A chains.

Cysteine knots are dimerisation domains defined by the presence of six cysteine residues between which disulphide bridges form. The only absolutely conserved residues are the six cysteines, and spacing between them is highly variable, apart from between cysteines 2 and 3, and 5 and 6: C[x]C[1-3x]GxC[x]C[x]CxC. The glycine between cysteines 2 and 3 is only present in a subset of cysteine knots. Drosophila slit and Human slit-1 both have an extra cysteine after cysteines 5 and 6: this may serve as an intermolecular bond.

Human Slit-1 gene displays the overall structure of the Drosophila gene, and amino acid conservation is found along the entire length of the protein (48% homology at the amino acid sequence excluding the signal sequence; see below). The Human gene has an extra LRR between LRR2 and LRR3 of the first set of LRRs; in the third set, the Human gene has an extra LRR between LRR3 and LRR4. The Human gene has two extra EGF repeats, on either side of the seventh EGF repeat in Drosophila slit.

Isolation of Human slit-1

Searching of the EST database revealed an EST, ab16g10.r1, with homology to the 99aa spacer region of Drosophila slit. This EST was used to probe a Human fetal brain library (Stratagene), and clones for Human slit-1 were isolated.

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Amino acid identity between *Drosophila* Slit and Human Slit-1

First amino-flanking sequence:	53%	
First set of Leucine Rich Repeats:	52%	(54%, 67%, NA, 38%, 54%, 50%)
First carboxy-flanking sequence:	42%	
Second amino-flanking sequence:	50%	
Second set of Leucine Rich Repeats:	60%	(54%, 58%, 67%, 71%, 50%)
Second carboxy-flanking sequence:	62%	
Third amino-flanking sequence:	56%	
Third set of Leucine Rich Repeats:	49%	(46%, 46%, 42%, NA, 58%)
Third carboxy-flanking sequence:	36%	
Fourth amino-flanking sequence:	53%	
Fourth set of Leucine Rich Repeats:	48%	(25%, 58%, 46%, 63%)
Fourth carboxy-flanking sequence:	63%	
First EGF repeat:	34%	
Second EGF repeat:	46%	
Third EGF repeat:	46%	
Fourth EGF repeat:	35%	
Fifth EGF repeat:	47%	
Spacer:	22%	
Sixth EGF repeat:	40%	
"99aa spacer":	38%	
Seventh EGF repeat:	11%/NA	
Eighth EGF repeat:	44%	
Ninth EGF repeat:	29%/NA	
Cysteine knot motif:	34%	

NA: not applicable due to absence of homologous repeat.
 Figures for individual LRRs are shown in brackets.

TABLE 5(A)

Hybridisation Probes for regions of Human Slit-1

Hybridisation Probe for the first Leucine rich repeat region

TGCCCGGCGCAGTGTCTTGTCTCGGGCAGCACAGTGGACTGTACAGGGCTGGCGCTGCGCAGCGTGCCAGGAAT	75
ATCCCCCGCAACACCGAGAGACTGGATTTAAATGGAATAACATCACAAGAATTACGAAGACAGATTTTGTGGT	150
CTTAGACATCTAAGAGTTCTTCAGCTTATGAGAATAAGATTAGCACCATTGAAAGAGGAGCATTCCAGGATCTT	225
AAAGAACTAGAGAGACTGCGTTTAAACAGAAATCACCTTCAGCTGTTTCTTGAGTTGCTGTTTCTTGGGACTGCG	300
AAGCTATACAGGCTTGATCTCAGTGAACCAAAATTCAGGCAATCCCAAGGAAAGCTTCCGTGGGGCAGTTGAC	375
ATAAAAAAATTGCAACTGGATTACAACCAGATCAGCTGTATTGAAGATGGGGCATTACAGGGCTCTCCGGGACCTG	450
GAAGTGCTCACTCTCAACAATAACAACATTACTAGACTTTCTGTGGCAAGTTTCAACCATATGCCATAAATTAGG	525
ACTTTTCGACTGCATTCAAACAACCTGTATTGTGACTGCCACCTGGCCTGGCTCTCCGACTGGCTTCGAAAAGG	600
CCTCGGGTTGTGTGTACACTCAGTGTATGGGCCCCCTCCACCTGAGAGGCCATAATGTAGCCGAGGTTCAAAAA	675
CGAGAATTTGTCTGCAGTGATGAGGAAGAAGTCCACAGTCATTATATGGCTCCTTCTGTAGTGTTTTGCAC	747

Hybridisation Probe for the second Leucine rich repeat region

TGCCCTGCCGCTGTACCTGTAGCAACAATATCGTAGACTGTCTGGGAAAGTCTCACTGAGATCCCCACAAT	75
CTTCCAGAGACCATCAGAGAAATACGTTTGAACAGAACACAATCAAAGTCATCCCTCCTGGAGCTTTCTACCA	150
TATAAAAGCTTAGACGAATTGACCTGAGCAATAATCAGATCTCTGAACCTGCACCAGATGCTTTCAAGGACTA	225
CGCTCTCTGAATTCATTGTCTCTATGGAATAAAATCACAGAACTCCCCAAAAGTTTATTTGAAGGACTGTTT	300
TCCTTACAGCTCCTATTATTGAATGCCAACAGATAAATGCTTCCGGGTAGATGCTTTTCAGGATCTCCACAAC	375
TTGAACCTTCTCTCCCTATATGACAACAAGCTTCAGACCATCGCCAAGGGGACCTTTTACCTCTTCGGGCCATT	450
CAAACTATGCATTGGCCCAAGACCCCTTTATTTGTGACTGCCATCTCAAGTGGCTAGCGGATTATCTCCATACC	525
AACCCGATTGAGACCACTGGTGCCCGTTGCACCAAGCCCCGCGCCTGGCAACAAAAGAATTGGACAGATCAAA	600
AGCAAGAAATTCGTTGTTTCAGGTACAGAAGATTATCGATCAAAATTAAGTGGAGACTGCTTTGCGGATCTGGCT	675

Hybridisation Probe for the third Leucine rich repeat region

TGCCCTGAAAAGTGTCTGTGAAGGAACACAGTAGATTGCTCTAATCAAAAGCTCAACAAAATCCCGGAGCAC	75
ATTCCCCAGTACACTGCAGAGTTGCGTCTCAATAATAATGAATTTACCGTGTGGAAGCCACAGGAATCTTTAAG	150
AAACTTCTCAATTACGTAATAAACTTTAGCAACAATAAGATCAGATATTGAGGAGGGAGCATTGAAGGA	225
GCATCTGGTGTAAATGAATACTTCTTACGTAATCTGTTTGGAAAATGTGCAGCATAAGATGTTCAAGGGATTG	300
GAAAGCCTCAAACTTTGATGTTGAGAAGCAATCGAATAACCTGTGTGGGGAATGACAGTTTCATAGGACTCAGT	375
TCTGTGCGTTTGTCTTTCTTTGTATGATAATCAAAATTACTACAGTTGCACCAGGGGCATTGATACTCTCCATTCT	450
TTATCTACTCTAAACCTCTTGCCCAATCTTTAACTGTAAGTGTACCTGGCTTGGTTGGGAGAGTGGCTGAGA	525
AAGAAGAGAAATTGTACCGGGAATCCTAGATGTCAAAAACCATACTTCCTGAAAGAAATACCCATCCAGGATGTG	600
GCCATTACAGACTTCACTTGTGATGACGGAATGATGACAATAGTTGCTCCCCACTTTCTCGC	663

Hybridisation Probe for the fourth Leucine rich repeat region

TGTCTACTGAATGTACTTGTCTGGATACAGTCGTCCGATGTAGCAACAAGGGTTGAAGGTCTTGCCGAAAGGT	75
ATTCCAAGAGATGTCACAGAGTTGTATCTGGATGGAACCAATTTACACTGGTTCCCAAGGAACTCTCCAACATAC	150
AAACATTTAACAATTATAGACTTAAGTAACAACAGAATAAGCACGCTTTCTAATCAGAGCTTCAGCAACATGACC	225
CAGTCCTCACCTTAATCTTAGTTACAACCGTCTGAGATGTATTCTCTCGCACCTTTGATGGATTAAAGTCT	300
CTTCGATTACTTTCTCTAGATGGAATGACATTTCTGTTGTGCTGAGGTTGCTTCAATGATCTTTCTGCATTA	375
TCACATCTAGCAATTGGAGCCAACCTCTTTACTGTGATTGTAACATGCAGTGGTTATCCGACTGGGTGAAGTCG	450
GAATATAAGGAGCCTGGAATTGCTCGTTGTGCTGGTCTGGAGAAATGGCAGATAAACTTTACTCACAACCTCC	525
TCCAAAAAATTTACCTGCAAGGTCTGTGGATGTCAATATTCTAGCTAAGTGTAAACCC	585

Hybridisation Probe for EGF repeats one to five

TGCCTATCAAATCCGTGTAAAAATGATGGCACATGTAATAGTGATCCAGTTGACTTTTACCGATGCACCTGTCCA	75
TATGGTTTCAAGGGGAGGACTGTGATGTCCCAATTCATGCCTGCATCAGTAACCCATGTAAACATGGAGGAAT	150
TGCCACTTAAAGGAAGGAGAAGAAGATGGATTCTGGTGTATTGTGCTGATGGATTGAAGGAGAAAATTGTGAA	225
GTCAACGTTGTGATGATTGTAAGATAAGTACTGTAATAATTTACATGTGTCGATGGCATTAAATACTACACA	300
TGCTTTTGGCCACTGAGTATACAGGTGAGTTGTGTGAGGAGAAGCTGGACTTCTGTGCCAGGACCTGAACCCC	375
TGCCAGCACGATTCAAAGTGCATCCTAACTCCAAAGGGATTCAAATGTGACTGCACACCAGGGTACGTAGGTGAA	450
CACTGCGACATCGATTTTGACGACTGCCAAGACAACAAGTGTAAAAACGGAGCCCACTGCACAGATGCAGTGAAC	525
GGCTATACGTGCATATGCCCGAAGGTTACAGTGGCTTGTCTGTGAGTTT	576

TABLE 5(B)

Hybridisation Probe for the sixth EGF repeat and preceding spacer region

TCTCCACCCATGGTCCTCCCTCGTACCAGCCCCTGTGATAATTTTGATTGTCAGAATGGAGCTCAGTGATCGTC 75
AGAATAAATGAGCCAATATGTCAGTGTTTGCCTGGCTATCAGGGAGAAAAGTGTGAAAA 134

Hybridisation Probe for the 99aa spacer/G-loop region

ATTGGTTAGTGTGAATTTTATAAACAAAGAGTCTTATCTTCAGATTCTTCAGCCAAGGTTTCGGCCTCAGACGAA 75
CATAACACTTCAGATTGCCACAGATGAAGACAGCGGAATCCTCCTGTATAAGGGTGACAAAGACCATATCGCGGT 150
AGAACTCTATCGGGGGCGTGTTCGTGCCAGCTATGACACCGGCTCTCATCCAGCTTCTGCCATTTACAGTGTGGA 225
GACAATCAATGATGGAACTTCCACATTGTGGAATCTTGCCTTGGATCAGAGTCTCTCTTTGTCCGTGGATGG 300
TGGGAACCCCAAAATCATCACTAATTGTCAAAGCAGTCCACTCTGAATTTTGAATCTCCACTCTATGTAGGAGG 375
CATGCCAGGGAAGAGTAACGTGGCATCTCTGCGCCAGGCCCCTGGGCAGAACGGAACAGCTTCCACGGCTGCAT 450
CCGGAACCTTTACATCAACAGTGAGCTGCAGGACTTCCAGAAGGTGCCGATGCAAACAGGCATTTTGCCTGGCTGT 526

Hybridisation Probe for EGF repeats seven to nine

GAGCCATGCCACAAGAAGGTGTGTGCCCATGACATGCCAGCCCAGCAGCCAGGCAGGCTTCACCTGCGAGTGC 75
CAGGAAGGATGGATGGGGCCCCTCTGTGACCAACGGACCAATGACCCTTGCCTTGGAAATAAATGCGTACATGGC 150
ACCTGCTTGCCCATCAATGCGTTCTCCTACAGCTGTAAGTGCTTGGAGGGCCATGGAGGTGTCTCTGTGATGAA 225
GAGGAGGATCTGTTTAAACCATGCCAGGCGATCAAGTGAAGCATGGGAAGTGCAGGCTTTCAGGCTTGGGGCAG 300
CCCTACTGTGAATGCAGCAGTGGATACACGGGGACAGCTGTGATCGAGAAATC 353

Hybridisation Probe for the cysteine knot region

TCTTGTCGAGGGGAAAGGATAAGAGATTATTACCAAAAGCAGCAGGGCTATGCTGCTTGCCAAACAACCAAGAAG 75
GTGTCCCGATTAGAGTGCAGAGGTGGGTGTGCAGGAGGGCAGTGCTGTGGACCGCTGAGGAGCAAGCGGCGGAAA 150
TACTCTTTTCAATGCACTGACGGCTCCTCCTTTGTGGACGAGGTTGAGAAAGTGGTGAAGTGCAGGCTGTACGAGG 225
TGTGTGTCC 234

BBEFT-443T6T6D

PCR Primers for regions of Human Slit-1**PCR Primers for the first Leucine rich repeat region**

Forward: 5' TCCCCGGCGCAGTGTCTTCTCGGGCAGC 3'
 Reverse: 5' GTGCAAAACACTACAAGAAGGAGCCATAAA 3'

PCR Primers for the second Leucine rich repeat region

Forward: 5' TGCCCTGCCGCCTGTACCTGTAGCAACAAT 3'
 Reverse: 5' AGCCAGATCCGCAAAGCAGTCTCCACTTAA 3'

PCR Primers for the third Leucine rich repeat region

Forward: 5' TGCCCTGAAAAGTGTGCTGTGAAGGAACC 3'
 Reverse: 5' GCGAGAAAGTGGGAGCAACTATTGTCATC 3'

PCR Primers for the fourth Leucine rich repeat region

Forward: 5' TGTCTACTGAATGTACTTGCTTGGATACA 3'
 Reverse: 5' GGGGTTACACTTAGCTAGAATATTGACATC 3'

PCR Primers for EGF repeats one to five

Forward: 5' TGCCTATCAAATCCGTGTAAAAATGATGGC 3'
 Reverse: 5' AAACCTACAGAACAGCCACTGTAACTTC 3'

PCR Primers for the sixth EGF repeat and preceding spacer region

Forward: 5' TCTCCACCCATGGTCTCCCTCGTACCAGC 3'
 Reverse: 5' TTTTCACACTTTTCTCCCTGATAGCCAGGC 3'

PCR Primers for the 99aa spacer/G-loop region

Forward: 5' ATTGGTTAGTGTGAATTTATAAACAAAGA 3'
 Reverse: 5' ACAGCCAGGCAAATGCCTGTTTGCATCGG 3'

PCR Primers for EGF repeats seven to nine

Forward: 5' GAGCCATGCCACAAGAAGGTGTGTGCCCAT 3'
 Reverse: 5' GATTTCTCGATCACAGCTGTCCCCGTGTAT 3'

PCR Primers for the cysteine knot region

Forward: 5' TCTTGTCGAGGGGAAAGGATAAGAGATTAT 3'
 Reverse: 5' GGACACACCTCGTACAGCCGCACTTCAC 3'

Table 3
a. Alignment of

sequences

Slit sequences

9/2/99

1	M A A P S R T T L M P P P F R L Q L R L - L I L P I L L L R H D A V H A E P Y	D-Slit
1	M R G V G W Q - - - - - M L S L S L G L V L A I L - - - - -	H-Slit1
40	S G G F G S S A V S S G G L G S V G I H I P G G G V G V I T E A R C P R V C S C	D-Slit
21	- - - - - - - - - - - - - - - N K V A P Q A C P A Q C S C	H-Slit1
80	T G L N V D C S H R G L T S V P R K I S A D V E R L E L Q G N N L T V I Y E T D	D-Slit
35	S G S T V D C H G L A L R S V P R N I P R N T E R L D L N G N N I T R I T K T D	H-Slit1
120	F Q R L T K L R M L Q L T D N Q I H T I E R N S F Q D L V S L E R L - - - - -	D-Slit
75	F A G L R H L R V L Q L M E N K I S T I E R G A F Q D L K E L E R L R L N R N H	H-Slit1
1	H L R V L Q L M E N R I S T I E R G A F Q D L K E L E R L R L N R N N	M-Slit1
154	- - - - - - - - - - - - - D I S N N V I T T V G R R V F K G A Q S L R	D-Slit
115	L Q L F P E L L F L G T A K L Y R L D L S E N Q I Q A I P R K A F R G A V D I K	H-Slit1
36	L Q L F P E L L F L G T A R L Y R L D L S E N Q I Q A I P R K A F R G A V D I K	M-Slit1
176	S L Q L D N N Q I T C L D E H A F K G L V E L E I L T L N N N N L T S L P H N I	D-Slit
155	N L Q L D Y N Q I S C I E D G A F R A L R D L E V L T L N N N N I T R L S V A S	H-Slit1
76	N L Q L D Y N Q I S C I E D G A F R A L R D L E V L T L N N N N I T R L S V A S	M-Slit1
216	F G G L G R L R A L R L S D N P F A C D C H L S W L S R F L R S A T R L A P Y T	D-Slit
195	F N H M P K L R T F R L H S N N L Y C D C H L A W L S D W L R K R P R V G L Y T	H-Slit1
116	F N H M P K L R T F R L H S N N L Y C	M-Slit1
256	R C Q S P S Q L K G Q N V A D L H D Q E F K C S G L T E - H A P M - - - E C G A	D-Slit
235	Q C M G P S H L R G H N V A E V Q K R E F V C S D E E E G H Q S F M A P S C S V	H-Slit1
292	E N S C P H P C R C A D G I V D C R E K S L T S V P V T L P D D T T D V R L E Q	D-Slit
275	L H - C P A A C T C S N N I V D C R G K G L T E I P T N L P E T I T E I R L E Q	H-Slit1
1	S P C T C S N N I V D C R G K G L M E I P A N L P E G I V E I R L E Q	H-Slit2
332	N F I T E L P P K S F S S F R R L R R I D L S N N N I S R I A H D A L S G L K Q	D-Slit
314	N T I K V I P P G A F S P Y K K L R R I D L S N N Q I S E L A P D A F Q G L R S	H-Slit1
36	N S I K A I P A G A F T Q Y K K L K R I D I S K N O I S D I A P D A F O G L K S	H-Slit2
372	L T T L V L Y G N K I K D L P S G V F K G L G S L R L L L L N A N E I S C I R K	D-Slit
354	L N S L V L Y G N K I T E L P K S L F E G L F S L Q L L L L N A N K I N C L R V	H-Slit1
76	L T S L V L Y G N K I T E I A K G L F D G L V S L Q L L L L	H-Slit2
1		CE-Slit
412	D A F R D L H S L S L L S L Y D N N I Q S L A N G T F D A M K S M K T V H L A K	D-Slit
394	D A F Q D L H N L N L L S L Y D N K L Q T I A K G T F S P L R A I Q T M H L A Q	H-Slit1
2	N P X I C D C N L Q W L A Q I N L Q K N I E T S G A R C E Q P K R L R K K K F A	CE-Slit
452	N P F I C D C N L R W L A D Y L H K N P I E T S G A R C E S P K R M H R R R I E	D-Slit
434	N P F I C D C H L K W L A D Y L H T N P I E T S G A R C T S P R R L A N K R I G	H-Slit1
42	T L P P N K F K C K G S E S F V S M Y A D S C F I D S I C P T Q C D C Y G T T V	CE-Slit
492	S L R E E K F K C S - W G E L R M K L S G E C R M D S D C P A M C H C E G T T V	D-Slit
474	Q I K S K K F R C S G T E D Y R S K L S G D C F A D L A C P E K C R C E G T T V	H-Slit1

dis
216
195
116
256
235
292
275
1
332
314
36
372
354
76
1
412
394
2
452
434
42
492
474

82	DCNKRG	LN	TI	PT	TS	IP	RF	AT	QL	LL	SG	NN	IS	TV	DL	NS	NI	HV	L	CE-Slit			
531	DCTGR	RL	KE	IP	RD	IP	LH	TE	LL	LN	DN	EL	GR	IS	SD	GL	FG	RL		D-Slit			
514	DCSNQK	LN	KI	PE	HI	PQ	YT	AE	LR	NN	NE	FT	VL	EA	TG	IF	KK	L		H-Slit1			
122	ENLEX	LD	LS	NN	HI	TF	IN	DK	SF	EK	LS	KL	RE	LX	LN	D				CE-Slit			
571	PHLV	KLE	LR	NQ	LT	GI	EP	NA	FE	GA	SH	IQ	EL	QL	GE	NN	KI	KE	I	D-Slit			
554	PQLR	KIN	FS	NN	KI	TD	IE	EG	AF	EG	AS	GV	NE	IL	LT	SN	RL	EN	V	H-Slit1			
1							EG	AF	NG	AA	SV	QEL	ML	TG	NN	QLE	TV			H-Slit2			
611	SNKMF	-	-	-	-	-	-	-	-	-	-	-	-	-	-	LG	LH	QK	TL	N	D-Slit		
594	QHKMF	KG	-	LES	LK	TL	ML	RS	NR	IT	CV	GN	DS	FI	GL	SS	VR	LL	LS		H-Slit1		
24	HGRGF	FR	GG	LS	G	LK	TL	ML	RS	NL	IG	CV	S	ND	TF	AG	LS	SS	VR	LL	H-Slit2		
626	LYDNQ	IS	CV	MP	GS	FE	HL	NS	LT	SL	NL	AS	NP	FN	CN	CH	LA	W	-	F	D-Slit		
633	LYDNQ	IT	TV	AP	GA	FD	TL	HS	LT	SL	NL	LA	NP	FN	CN	CH	LA	W	-	L	H-Slit1		
64	LYDN	RIT	TT	IT	PG	AF	TL	V	SL	ST	IN	LL	SN	PF	FN	CN	CH	LA	W	-	H-Slit2		
665	AECV	RKK	SL	NG	GA	AR	CG	AP	SK	VR	DV	QI	KD	LP	HS	EF	KC	SS	SE		D-Slit		
672	GEWLR	KKR	IV	T	GN	PR	CQ	KPY	FL	KE	IP	IQ	DV	AI	QD	FT	CD	DG		H-Slit1			
104	GKWL	RKR	IV	S	GN	PR	CQ	KPF	FL	KE	IP	IQ	GV	GH	PG	I				H-Slit2			
1																							
705	NSE	-	G	CL	GD	GY	CP	PS	CT	CT	TG	TV	VA	AC	SR	NQ	LK	EIP	RG	IP	AE	CE-Slit	
712	NDDNS	CS	PL	SR	CP	TE	CT	CL	D	TV	VR	CS	NK	GL	KV	LP	KG	IP	RD		D-Slit		
																					H-Slit1		
16	TELY	LD	AN	YI	NE	IP	AH	DL	NR	LY	SL	TK	LD	LS	HN	RL	IS	LEN			CE-Slit		
744	TELY	LE	SN	IE	EQ	IHY	ER	IR	HL	RS	LT	RL	DL	LS	NN	QI	TI	LS	N		D-Slit		
752	TELY	LD	GN	QF	TL	VP	KE	-	LS	NY	KH	LT	LI	DL	LS	NN	RI	ST	LS	N	H-Slit1		
56	NTFS	NL	TR	LS	TL	LI	SY	NK	LR	CL	QP	LA	FN	GL	NA	LR	IL	SL	HG		CE-Slit		
784	YTF	AN	LT	KL	ST	LI	SY	NK	LQ	CL	QR	HA	LS	GL	NN	LR	VR	VS	SL	HG	D-Slit		
791	QSFS	NM	TQ	LL	TL	LI	LS	NR	LR	CI	PP	RT	FD	GL	KS	LR	LL	SL	HG		H-Slit1		
96	NDIS	F	LP	QS	AF	SN	LT	SI	TH	IA	V	GS	NS	SL	YCD	CNM	AW	FS	SK	WI	CE-Slit		
824	NRIS	ML	PE	GS	FE	DL	KS	SL	TH	IA	L	GS	NP	LY	CD	CGL	KW	FS	SD	WI	D-Slit		
831	NDIS	V	V	PE	GA	FN	DL	SA	LS	HL	AI	GA	NP	LY	CD	CNM	QW	LS	SD	WV	H-Slit1		
136	KSKF	I	E	AG	IAR	CE	YP	NT	VS	NQ	LL	LT	AP	YQ	FT	CD	SK	VP	TK		CE-Slit		
864	KLDY	V	EP	GI	AR	CA	EP	EQ	M	KD	KL	IL	ST	PS	SS	FV	CR	GR	VR	ND	D-Slit		
871	KSEY	K	EP	GI	AR	CA	G	P	G	EM	AD	KL	LL	LT	PS	SK	K	FT	CQ	GP	V	H-Slit1	
176	LATK	CD	LD	CL	NS	SP	CK	NN	AI	CE	TT	SS	SR	KY	TC	NC	TP	GF	YGV	H	CE-Slit		
904	ILAK	CN	AC	FE	QP	CQ	NQ	QA	QC	VA	LP	QR	EY	QC	LC	QP	GY	HG	KHC		D-Slit		
911	ILAK	CN	PC	LS	NP	CK	ND	GT	CN	SD	PD	VF	YR	CT	CP	YG	FK	GQ	DC		H-Slit1		
216	ENQ	ID	AC	YG	SP	CL	NN	AT	CK	V	-	-	AQ	AG	RF	NC	YC	NK	GF	EG	DY	CE-Slit	
944	EFM	ID	AC	YG	NP	CR	NN	AT	CT	VL	E	-	-	EG	RF	SC	QC	AP	GY	TGAR		D-Slit	
951	DVP	TH	AC	IS	NP	CK	HG	GT	CH	LK	EG	E	ED	GF	WC	IC	AD	GF	EG	EN	H-Slit1		
254	CEK	N	IDD	CV	-	NS	K	CEN	G	G	K	CV	D	L	V	R	FC	SE	EL	KNF	QSF	QIN	CE-Slit
982	CET	N	IDD	CL	GE	IK	CQ	NN	AT	CID	-	-	-	-	-	-	-	-	-	-	-	GVE	D-Slit
991	CEV	N	V	DD	C	-	ED	ND	C	ENN	S	TC	VD	-	-	-	-	-	-	-	-	GIN	H-Slit1

293	S Y R C D C P M E Y E G K H C E D K L E Y C T K K L N P C E N N G K C I P I N G	CE-Slit
1007	S Y K C E C Q P G F S G E F C D T K I Q F C S P E F N P C A N G A K C M D H F T	D-Slit
1015	N Y T C L C P P E Y T G E L C E E K L D F C A Q D L N P C Q H D S K C I L T P K	H-Slit1
1		M-Slit2
		D P L P V
333	S Y S C M C S P G F T G N N C E T N I D D C K N V E C Q N G G S C V D G I L S Y	CE-Slit
1047	H Y S C D C Q A G F H G T N C T D N I D D C Q N H M C Q N G G T C V D G I N D Y	D-Slit
1055	G F K C D C T P G Y V G E H C D I D F D D C O D N K C K N G A H C T D A V N G Y	H-Slit1
1		M-Slit1
1	W P R C E C M P G Y A G D N C S E N Q D D C R D H R C Q N G A Q C M D E V N S Y	H-Slit2
6	H H R C E C M L G Y T G D N C S E N Q D D C K D H K C Q N G A Q C V D E V N S Y	M-Slit2
373	D C L C R P G Y A G Q Y C E I P P M M D H E Y Q K T D A C Q Q S A C G Q G - E C	CE-Slit
1087	Q C R C P D D Y T G K Y C E G H N M I S M M Y P Q T S P C Q N H E C K H G V - C	D-Slit
1095	T C I C P E G Y S G L F C E F S P - - P M V L P R T S P C D N F D C Q N G A Q C	H-Slit1
24	T C I C P Q G F S G L F C E H P P - - P M V L L Q T S P C D Q Y E C Q N G A Q C	M-Slit1
41	S C L C A E G Y S G Q L C E I P P - - H L P A P K - S P C E G T E C Q N G A N C	H-Slit2
46	A C L C V E G Y S G Q L C E I P P - - - - A P R - S S C E G T E C Q N G A N C	M-Slit2
412	V A S Q N - S S D F T C K C H E G F S G P S C D R Q M S V G F K N P G A Y L A L	CE-Slit
1126	F Q P N A Q G S D Y L C R C H P G Y T G K W C E Y L T S I S F V H N N S F V E L	D-Slit
1133	I V R I N E P - - - I C Q C L P G Y Q G E K C E K L V S V N F I N K E S Y L Q I	H-Slit1
62	I V V Q Q E P - - - T C R C P P G F A G P R C E K L I T V N F V G K D S Y V E L	M-Slit1
98	V D Q G N R P - - - V C Q C L P G F G G P E C E K L L S V N F V D R D T Y L Q F	H-Slit2
80	V D Q G S R P - - - V C Q C L P G F G G P E C E K L L S V N F V D R D T Y L Q F	M-Slit2
451	D P L A S - - D G T I T M T L R T T S K T G I L L Y Y G D D H F V S A E L Y D G	CE-Slit
1166	E P L R T R P E A N V T I V F S S A E Q N G I L M Y D G Q D A H L A V E L F N G	D-Slit
1170	P S A K V R P Q T N I T L Q I A T D E D S G I L L Y K G D K D H I A V E L Y R G	H-Slit1
99	A S A K V R	M-Slit1
115	T D L Q N W X R X N I T L Q V F T A E D N G I L L Y N G G N D H I A V X L Y X G	H-Slit2
117	T D L Q N W P R A N I T L Q V S T A E D N G I L L Y N G D N D H I A V E L Y	M-Slit2
489	R V K L V Y Y I G N F P A S H M Y S S V K V N D G L P H R I S I R T S E R K C F	CE-Slit
1206	R I R V S Y D V G N H P V S T M Y S F E M V A D G K Y H A V E L L A I K K N F T	D-Slit
1210	R V R A S Y D T G S H P A S A I Y S V E T I N D G N F H I V E L L A L D Q S L S	H-Slit1
155	H V R F S Y	H-Slit2
529	L Q I D K N P V Q I V E N S G K S D Q L I T K G K E M L Y I G G L P I E K S Q D	CE-Slit
1246	L R V D R G L A R S I I N E G S N D Y L - - K L T T P M F L G G L P V D P A Q Q	D-Slit
1250	I S V D G G N P K I I T N L S K Q S T L - - N F D S P L Y V G G M P G K S N V A	H-Slit1
1		M-Slit1
		I L D V A
569	A K R R F H V K N S E S L K G C I S S I T I N E V P I N L Q Q A L E N V N T E Q	CE-Slit
1284	A Y K N W Q I R N L T S F K G C M K E V W I N H K L V D F G N A Q R Q Q K I T P	D-Slit
1288	S L R Q A P G Q N G T S F H G C I R N L Y I N S E L Q D F Q K V P M Q T G I L P	H-Slit1
6	S L R Q A P G E N G T S F H G C I R N L Y I N S E L Q D F R K M P M Q T G I L P	M-Slit1
609	S C -	CE-Slit
1324	G C A L - - - - - L E G E Q Q E E E D D E Q D F M D E - - - - - T P H I K E E P	D-Slit
1328	G C E P C H K K V C A H G T C Q P S S Q A G F T C E C Q E G W M G P L C D Q R T	H-Slit1
46	G C E P C H K K V C A H G C C Q P S S Q S G F T C E C E E G W M G P L C D Q R T	M-Slit1

a Table 2
~~Table 4~~

Alignment of Drosophila Slit and Human Slit-1

1	M	A	A	P	S	R	T	T	L	M	P	P	P	F	R	L	Q	L	R	L	-	L	I	L	P	I	L	L	L	L	R	H	D	A	V	H	A	E	P	Y	D-Slit		
1	M	R	G	V	G	W	Q	-	-	-	-	-	-	-	M	L	S	L	S	L	G	L	V	L	A	I	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	H-Slit1	
40	S	G	G	F	G	S	S	A	V	S	S	G	G	L	G	S	V	G	I	H	I	P	G	G	G	V	G	V	I	T	E	A	R	C	P	R	V	C	S	C	D-Slit		
21	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	K	V	A	P	Q	A	C	P	A	Q	C	S	C	H-Slit1
80	T	G	L	N	V	D	C	S	H	R	G	L	T	S	V	P	R	K	I	S	A	D	V	E	R	L	E	L	Q	G	N	N	L	T	V	I	Y	E	T	D	D-Slit		
35	S	G	S	T	V	D	C	H	G	L	A	L	R	S	V	P	R	N	I	P	R	N	T	E	R	L	D	L	N	G	N	N	I	T	R	I	T	K	T	D	H-Slit1		
120	F	Q	R	L	T	K	L	R	M	L	Q	L	T	D	N	Q	I	H	T	I	E	R	N	S	F	Q	D	L	V	S	L	E	R	L	-	-	-	-	-	-	D-Slit		
75	F	A	G	L	R	H	L	R	V	L	Q	L	M	E	N	K	I	S	T	I	E	R	G	A	F	Q	D	L	K	E	L	E	R	L	R	L	N	R	N	H	H-Slit1		
154	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D-Slit			
115	L	Q	L	F	P	E	L	L	F	L	G	T	A	K	L	Y	R	L	D	L	S	E	N	Q	I	Q	A	I	P	R	K	A	F	R	G	A	V	D	I	K	H-Slit1		
176	S	L	Q	L	D	N	N	Q	I	T	C	L	D	E	H	A	F	K	G	L	V	E	L	E	I	L	T	L	N	N	N	N	L	T	S	L	P	H	N	I	D-Slit		
155	N	L	Q	L	D	Y	N	Q	I	S	C	I	E	D	G	A	F	R	A	L	R	D	L	E	V	L	T	L	N	N	N	N	I	T	R	L	S	V	A	S	H-Slit1		
216	F	G	G	L	G	R	L	R	A	L	R	L	S	D	N	P	F	A	C	D	C	H	L	S	W	L	S	R	F	L	R	S	A	T	E	L	A	P	Y	T	D-Slit		
195	F	N	H	M	P	K	L	R	T	F	R	L	H	S	N	N	L	Y	C	D	C	H	L	A	W	L	S	D	W	L	R	K	R	P	R	V	G	L	Y	T	H-Slit1		
256	R	C	Q	S	P	S	Q	L	K	G	Q	N	V	A	D	L	H	D	Q	E	F	K	C	S	G	L	T	E	-	H	A	P	M	-	-	-	E	C	G	A	D-Slit		
235	Q	C	M	G	P	S	H	L	R	G	H	N	V	A	E	V	Q	K	R	E	F	V	C	S	D	E	E	E	G	H	Q	S	F	M	A	P	S	C	S	V	H-Slit1		
292	E	N	S	C	P	H	P	C	R	C	A	D	G	I	V	D	C	R	E	K	S	L	T	S	V	P	V	T	L	P	D	D	T	T	D	V	R	L	E	Q	D-Slit		
275	L	H	-	C	P	A	A	C	T	C	S	N	N	I	V	D	C	R	G	K	G	L	T	E	I	P	T	N	L	P	E	T	I	T	E	I	R	L	E	Q	H-Slit1		
332	N	F	I	T	E	L	P	P	K	S	F	S	S	F	R	R	L	R	R	I	D	L	S	N	N	N	I	S	R	I	A	H	D	A	L	S	G	L	K	Q	D-Slit		
314	H	T	I	K	V	I	P	P	G	A	F	S	P	Y	K	K	L	R	R	I	D	L	S	N	N	Q	I	S	E	L	A	P	D	A	F	Q	G	L	R	S	H-Slit1		
372	L	T	T	L	V	L	Y	G	N	K	I	K	D	L	P	S	G	V	F	K	G	L	G	S	L	R	L	L	L	L	N	A	N	E	I	S	C	I	R	K	D-Slit		
354	L	N	S	L	V	L	Y	G	N	K	I	T	E	L	P	K	S	L	F	E	G	L	F	S	L	Q	L	L	L	L	N	A	N	K	I	N	C	L	R	V	H-Slit1		
412	D	A	F	R	D	L	H	S	L	S	L	L	S	L	Y	D	N	N	I	Q	S	L	A	N	G	T	F	D	A	M	K	S	M	K	T	V	H	L	A	K	D-Slit		
394	D	A	F	Q	D	L	H	N	L	N	L	L	S	L	Y	D	N	K	L	O	T	I	A	K	G	T	F	S	P	L	R	A	I	Q	T	M	H	L	A	Q	H-Slit1		
452	N	P	F	I	C	D	C	N	L	R	W	L	A	D	Y	L	H	K	N	P	I	E	T	S	G	A	R	C	E	S	P	K	R	M	H	R	R	R	I	E	D-Slit		
434	N	P	F	I	C	D	C	H	L	K	W	L	A	D	Y	L	H	T	N	P	I	E	T	S	G	A	R	C	T	S	P	R	R	L	A	N	K	R	I	G	H-Slit1		
492	S	L	R	E	E	K	F	K	C	S	-	W	G	E	L	R	M	K	L	S	G	E	C	R	M	D	S	D	C	P	A	M	C	H	C	E	G	T	T	V	D-Slit		
474	Q	I	K	S	K	K	F	R	C	S	G	T	E	D	Y	R	S	K	L	S	G	D	C	F	A	D	L	A	C	P	E	K	C	R	C	E	G	T	T	V	H-Slit1		
531	D	C	T	G	R	R	L	K	E	I	P	R	D	I	P	I	H	T	T	E	L	L	N	D	N	E	L	G	R	I	S	S	D	G	L	F	G	R	L	D-Slit			
514	D	C	S	N	Q	K	L	N	K	I	P	E	H	I	P	Q	Y	T	A	E	L	R	L	N	N	N	E	F	T	V	L	E	A	T	G	I	F	K	K	L	H-Slit1		
571	P	H	L	V	K	L	E	L	K	R	N	Q	L	T	G	I	E	P	N	A	F	E	G	A	S	H	I	Q	E	L	Q	L	G	E	N	K	I	K	E	I	D-Slit		
554	P	Q	L	R	K	I	N	F	S	N	N	K	I	T	D	I	E	E	G	A	F	E	G	A	S	G	V	N	E	I	L	L	T	S	N	R	L	E	N	V	H-Slit1		
611	S	N	K	M	F	L	G	L	H	Q	L	K	T	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	L	D-Slit	
594	Q	H	K	M	F	K	G	L	E	S	L	K	T	L	M	L	R	S	N	R	I	T	C	V	G	N	D	S	F	I	G	L	S	S	V	R	L	L	S	L	H-Slit1		
627	Y	D	N	Q	I	S	C	V	M	P	G	S	F	E	H	L	N	S	L	T	S	L	N	L	A	S	N	P	F	N	C	N	C	H	L	A	W	F	A	E	D-Slit		
634	Y	D	N	Q	I	T	T	V	A	P	G	A	F	D	T	L	H	S	L	S	T	L	N	L	L	A	N	P	F	N	C	N	C	Y	L	A	W	L	G	E	H-Slit1		

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667 C V R R K K S L N G G A A P S K V R D V Q I K D L P H K C S S E N S D-Slit
.674 W L R R K K R I V T G N F R C Q K P Y F L K E I P I Q D V A I Q D F T C D D G N D H-Slit1

707 E - G C L G D G Y C P P S C T C T G T V V A C S R N Q L K E I P R G I P A E T S D-Slit
714 D N S C S P L S R C P T E C T C L D T V V R C S N K G L K V L P K G I P R D V T H-Slit1

746 E L Y L E S N E I E Q I H Y E R I R H L R S L T R L D L S N N Q I T I L S N Y T D-Slit
754 E L Y L D G N Q F T L V P K E - L S N Y K H L T L I D L S N N R I S T L S N Q S H-Slit1

786 F A N L T K L S T L I I S Y N K L Q C L Q R H A L S G L N N L R V V S L H G N R D-Slit
793 F S H M T Q L L T L I L S Y M R L R C I P P R T F D G L K S L R L L S L H G N D H-Slit1

826 I S M L P E G S F E D L K S L T H I A L G S N P L Y C D C G L K W F S D W I K L D-Slit
833 I S V V P E G A F N D L S A L S H L A I G A N P L Y C D C N M Q W L S D W V K S H-Slit1

866 D Y V E P G I A R C A E P E Q M K D K L I L S T P S S S F V C R G R V R N D I L D-Slit
873 E Y K E P G I A R C A G P G E M A D K L L L T T P S K K F T C Q G P V D V N I L H-Slit1

906 A K C N A C F E Q P C Q N Q A Q C V A L P Q R E Y Q C L C Q P G Y H G K H C E F D-Slit
913 A K C N P C L S N P C K N D G T C N S D P V D F Y R C T C P Y G F K G Q D C D V H-Slit1

946 M I D A C Y G N P C R N N A T C T V L E - - E G R F S C Q C A P G Y T G A R C E D-Slit
953 P I H A C I S N P C K H G G T C H L K E G E E D G F W C I C A D G F E G E N C E H-Slit1

984 T H I D D C L G E I K C Q N N A T C I D G V E S Y K C E C Q P G F S G E F C D T D-Slit
993 V M V D D C - E D N D C E N N S T C V D G I N N Y T C L C P P E Y T G E L C E E H-Slit1

1024 K I Q F C S P E F H P C A N G A K C M D H F T H Y S C D C Q A G F H G T N C T D D-Slit
1032 K L D F C A Q D L H P C Q H D S K C I L T P K G F K C D C T P G Y V G E H C D I H-Slit1

1064 N I D D C Q N H M C Q H G G T C V D G I N D Y Q C R C P D D Y T G K Y C E G H N D-Slit
1072 D F D D C Q D N K C K M G A H C T D A V H G Y T C I C P E G Y S G L F C E F S P H-Slit1

1104 M I S M M Y P Q T S P C Q H H E C K H G V - C F Q P N A Q G S D Y L C R C H P G D-Slit
1112 - - P M V L P R T S P C D H F D C Q N G A Q C I - - - V R I N E P I C Q C L P G H-Slit1

1143 Y T G K W C E Y L T S I S F V H N N S F V E L E P L R T R P E A H V T I V F S S D-Slit
1147 Y Q G E K C E K L V S V N F I N K E S Y L Q I E S A K V R P Q T N I T L Q I A T H-Slit1

1183 A E Q N G I L M Y D G Q D A H L A V E L F N G R I R V S Y D V G N H P V S T M Y D-Slit
1187 D E D S G I L L Y K G D K D H I A V E L Y R G R V R A S Y D T G S H P A S A I Y H-Slit1

1223 S F E M V A D G K Y H A V E L L A I K K N F T L R V D R G L A R S I I H E G S N D-Slit
1227 S V E T I N D G N F H I V E L L A L D Q S L S L S V D G G N P K I I T H L S K Q H-Slit1

1263 D Y L K L T T P M F L G G L P V D P A Q Q A Y K N W Q I R N L T S F K G C M K E D-Slit
1267 S T L N F D S P L Y V G G M P G K S N V A S L R Q A P G Q N G T S F H G C I R N H-Slit1

1303 V W I N H K L V D F G N A Q R Q Q K I T P G C A L - - - L E G E Q Q E E E D D D-Slit
1307 L Y I N S E L Q D F Q K V P M Q T G I L P G C E P C H K K V C A H G T C Q P S S H-Slit1

1339 E Q D F M D E - - - - - T P H I K E E P V D P C L E N K C R R G S R C V P N S D-Slit
1347 Q A G F T C E C Q E G W M G P L C D Q R T N D P C L G N K C V H G T - C L P I N H-Slit1

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1373	N A R D G Y Q C K C K H G I G R Y C D Q E G S T E P - - - - -	D-Slit
1386	A F - - S Y S C K C L E G H G G V L C D E E E D L F N P C Q A I K C K H G K C R	H-Slit1
1401	- - - - - P T V T A A S - - - - - T C R K E Q V R E Y Y T E N D -	D-Slit
1424	L S G L G Q P Y C E C S S G Y T G D S C D R E I S C R G E R I R D Y Y Q K Q Q G	H-Slit1
1423	- - - C R S R Q P L K Y A K C V G G C - G N Q C C A A K I V R R R K V R M V C S	D-Slit
1464	Y A A C Q T T K K V S R L E C R G G C A G G O C C G P L R S K R R K Y S F E C T	H-Slit1
1459	N N R K Y I K N L D I V R K C G C T K K C Y	D-Slit
1504	D G S S F V D E V E K V V K C G C T R - C V S	H-Slit1

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